

## RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/813,432

TIME: 10:23:19

Input Set : A:\Cura7291.APP

Output Set: N:\CRF3\08282001\I813432.raw

ENTERED

3 <110> APPLICANT: Taupier Jr., Raymond J  
4 Majmuder, Kamud  
5 Spaderna, Steven K  
6 Smithson, Glenda  
7 Mezes, Peter S  
8 Vernet, Corine A. M.  
10 <120> TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same  
12 <130> FILE REFERENCE: 15966-729  
14 <140> CURRENT APPLICATION NUMBER: 09/813,432  
15 <141> CURRENT FILING DATE: 2001-03-20  
17 <150> PRIOR APPLICATION NUMBER: 60/190,835  
18 <151> PRIOR FILING DATE: 2000-03-20  
20 <150> PRIOR APPLICATION NUMBER: 60/190,768  
21 <151> PRIOR FILING DATE: 2000-03-20  
23 <150> PRIOR APPLICATION NUMBER: 60/190,972  
24 <151> PRIOR FILING DATE: 2000-03-22  
26 <150> PRIOR APPLICATION NUMBER: 60/191,199  
27 <151> PRIOR FILING DATE: 2000-03-22  
29 <150> PRIOR APPLICATION NUMBER: 60/191,947  
30 <151> PRIOR FILING DATE: 2000-03-24  
32 <150> PRIOR APPLICATION NUMBER: 60/192,665  
33 <151> PRIOR FILING DATE: 2000-03-28  
35 <150> PRIOR APPLICATION NUMBER: 60/192,657  
36 <151> PRIOR FILING DATE: 2000-03-28  
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39 <151> PRIOR FILING DATE: 2000-03-28  
41 <150> PRIOR APPLICATION NUMBER: 60/192,664  
42 <151> PRIOR FILING DATE: 2000-03-28  
44 <150> PRIOR APPLICATION NUMBER: 60/192,836  
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47 <150> PRIOR APPLICATION NUMBER: 60/193,843  
48 <151> PRIOR FILING DATE: 2000-03-31  
50 <160> NUMBER OF SEQ ID NOS: 78  
52 <170> SOFTWARE: PatentIn Ver. 2.1  
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61 ctctgggtca aggctgtcag tgatggtgaa agcacaggaa tctgcctttt ttcccagaga 120  
62 ttctctcatga ttctttggct caaaggagtt gtcttcagtg tcacaactgt tgatctgaaa 180  
63 aggaacacctg cagatctgca aaacaaggct cctgggaacc acccaccact tataacttca 240  
64 acagtgaagt caaataagat tgaggaagct cctgaagaag tcttatgtcc tcccagtagc 300  
65 ttaaagcttt caccaaaaca ccagaaatca aatactgctg gaatggacat ctttgccaaa 360  
66 ttctctgcat acatcaagaa ttcaaggcca gaggttaatg aagcattagt gaagcatctc 420  
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70 aaatataaaa atatagaaaa aaaaggaatg actggcatct ggagatacct aacgaatata 660
71 agtagtaggg atatgttcaa caatacctgt cccaatgata aagagattga aatagcagca 720
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85           20           25           30
87 Gly Ile Cys Leu Phe Ser Gln Arg Phe Leu Met Ile Leu Trp Leu Lys
88           35           40           45
90 Gly Val Val Phe Ser Val Thr Val Asp Leu Lys Arg Lys Pro Ala
91           50           55           60
93 Asp Leu Gln Asn Lys Ala Pro Gly Asn His Pro Pro Leu Ile Thr Ser
94   65           70           75           80
96 Thr Val Lys Ser Asn Lys Ile Glu Glu Ala Pro Glu Glu Val Leu Cys
97           85           90           95
99 Pro Pro Lys Tyr Leu Lys Leu Ser Pro Lys His Pro Glu Ser Asn Thr
100          100          105          110
102 Ala Gly Met Asp Ile Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Ser
103          115          120          125
105 Arg Pro Glu Val Asn Glu Ala Leu Val Lys His Leu Leu Lys Thr Leu
106          130          135          140
108 Gln Lys Met Glu Tyr Leu Asn Ser Pro Leu Pro Asp Glu Ile Asp Glu
109 145          150          155          160
111 Asn Ser Met Gln Asp Thr Lys Phe Ser Thr His Lys Phe Leu Asn Gly
112          165          170          175
114 Asn Lys Met Ala Leu Ala Asp Cys His Leu Leu Pro Lys Leu His Ile
115          180          185          190
117 Val Lys Lys Lys Glu Lys Tyr Arg Lys Tyr Lys Asn Ile Glu Lys Lys
118          195          200          205
120 Gly Met Thr Gly Ile Trp Arg Tyr Leu Thr Asn Thr Ser Ser Arg Asp
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140 aaaaaaaggg tgctatggcc aaaaaagatt gtattagctt ttttgatggc aaaaacctca 300
141 ccataaaaaa ggagagtact ttaaaatcat acagttttct cacactcagg ggagggaaat 360
142 tcaaagaaac tacaggtgac ggcagaaaaa ctcagacttg cacctttaca tatggcacat 420
143 tggttcgaca tcagaagtgg aatggaaaagg aaggcaaaat aagaaaattg aaagacagga 480
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145 aataaaaact                                     550

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150 &lt;212&gt; TYPE: PRT

151 &lt;213&gt; ORGANISM: Homo sapiens

153 &lt;400&gt; SEQUENCE: 4

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157 Gln His Val Ser His Ala Gly Pro Cys Ser Ala His Ser Thr His Leu
158           20           25           30
160 Leu Thr Pro Thr Met Asp Thr Val Gln Gln Leu Glu Glu Arg Gly His
161           35           40           45
163 Leu Met Asp Ser Lys Gly Phe Asp Glu Asn Lys Tyr Met Lys Glu Leu
164           50           55           60
166 Gly Val Gly Leu Ala Leu Cys Glu Lys Lys Gly Ala Met Ala Lys Lys
167           65           70           75           80
169 Asp Cys Ile Ser Phe Phe Asp Gly Lys Asn Leu Thr Ile Lys Met Glu
170           85           90           95
172 Ser Thr Leu Lys Ser Tyr Ser Phe Leu Thr Leu Arg Gly Gly Lys Phe
173           100          105          110
175 Lys Glu Thr Thr Gly Asp Gly Arg Lys Thr Gln Thr Cys Thr Phe Thr
176           115          120          125
178 Tyr Gly Thr Leu Val Arg His Gln Lys Trp Asn Gly Lys Glu Gly Lys
179           130          135          140
181 Ile Arg Lys Leu Lys Asp Arg Lys Leu Val Val Asp Cys Ile Ile Asn
182 145          150          155          160
184 Asn Val Thr Cys Thr Gln Ile Tyr Glu Lys Val Glu
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188 &lt;210&gt; SEQ ID NO: 5

189 &lt;211&gt; LENGTH: 915

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191 &lt;213&gt; ORGANISM: Homo sapiens

193 &lt;400&gt; SEQUENCE: 5

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196 cgcggtgga tgcggtgct agcggagggc gagggctgcg ctccctgccg gccagaagag 180
197 tgcgcgcgc cgcggggctg cctggcgggc aggggtgcgc acgctgctgc ctgctgctgg 240
198 gaatgcgcca acctcgagg ccagctctgc gacctggacc ccagtgtca cttctacggg 300
199 cactgcggcg agcagcttga gtgcccggctg gacacaggcg gcgacctgag ccgcggagag 360
200 gtgccggaac ctctgtgtgc ctgtcgttcg cagagtccgc tctgcgggtc cgacgggtcac 420
201 acctactccc agatctgccg cctgcaggag gcggcccgcg ctgcggccga tgccaacctc 480
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204 gcctccatcg agtggaggaa ggatggcttg gacatccagc tgccagggga tgaccccccac 660
205 atctctgtgc agtttagggg tggaccccag aggtttgagg tgactggctg gctgcagatc 720
206 caggctgtgc gtcccagtga tgagggcact taccgctgcc ttggccgcaa tgccctgggt 780
207 caagtggagg cccctgctag cttgacagtg ctacacctg accagctgaa ctctacaggc 840
208 atcccccagc tgcgatcact aaacctgggt cctgaggagg aggctgagag tgaagagaat 900
209 gacgattact actag 915
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213 <211> LENGTH: 304
214 <212> TYPE: PRT
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217 <400> SEQUENCE: 6
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221 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro
222 20 25 30
224 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
225 35 40 45
227 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
228 50 55 60
230 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
231 65 70 75 80
233 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
234 85 90 95
236 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
237 100 105 110
239 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
240 115 120 125
242 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
243 130 135 140
245 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
246 145 150 155 160
248 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
249 165 170 175
251 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
252 180 185 190
254 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
255 195 200 205
257 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
258 210 215 220
260 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
261 225 230 235 240
263 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Arg
264 245 250 255
266 Asn Ala Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr
267 260 265 270
269 Pro Asp Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn
270 275 280 285
272 Leu Val Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr

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287 tggggggcctt ggggtcccaga tctccatgtc ctgttctacc agtttctggg gcggcttggg 180
288 gtctgggggc ctggccacag agatggctgg gggctctggca gaaatggggg gcatccagaa 240
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290 cctggagacc gagaactgga ggctggagag caaaatccag gagtatctgg agaagagacc 360
291 ccatgtcaga gactggggcc attacttcaa gaccatcaag gaactgaggg ctcatatctt 420
292 cgcaaatact gtggacaatg tccacatcat tctgcagatc gacaatgcc gtcttgctgc 480
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296 aaaaggcttg caagtccaga ttgccaactc tgggttggcc gtggaggtag atgccccaa 720
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305 gcaaaccatc caaaagacca ccaccgcca gatagtggat agcaaagtgg tgtctgagat 1260
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321 Ala Ser Ile Tyr Ala Gly Thr Gly Gly Leu Gly Ser Gln Ile Ser Met
322 35 40 45
324 Ser Cys Ser Thr Ser Phe Trp Gly Gly Leu Gly Ser Gly Gly Leu Ala
325 50 55 60
327 Thr Glu Met Ala Gly Gly Leu Ala Glu Met Gly Gly Ile Gln Asn Glu
328 65 70 75 80
330 Lys Glu Thr Met Gln Ser Leu Asn Asp His Leu Asp Tyr Leu Asp Arg
331 85 90 95
333 Val Arg Asn Leu Glu Thr Glu Asn Trp Arg Leu Glu Ser Lys Ile Gln
334 100 105 110
336 Glu Tyr Leu Glu Lys Arg Pro His Val Arg Asp Trp Gly His Tyr Phe
337 115 120 125

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